

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2002, 02:57:40 ; Search time 66 Seconds
(without alignments)
9325.762 Million cell updates/sec

Title: US-09-716-536-7

Perfect score: 2007

Sequence: 1 gtgcggtgagcgaatttgc.....aaaaaaaaaaaaaaaaa 2007

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/prodata/1/lna/5A_COMB.seq:*
2: /cgn2_6/prodata/1/lna/5B_COMB.seq:*
3: /cgn2_6/prodata/1/lna/6A_COMB.seq:*
4: /cgn2_6/prodata/1/lna/6B_COMB.seq:*
5: /cgn2_6/prodata/1/lna/CTUS_COMB.seq:*
6: /cgn2_6/prodata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2007	100.0	2007	4	US-09-052-089A-7
2	1890.8	94.2	2065	2	US-08-968-751-1
3	1062.8	53.0	1975	4	US-09-052-089A-8
4	176.4	8.8	7542	4	US-09-734-030-3
5	65.8	3.3	7218	1	US-08-232-463-14
6	52	2.6	3489	2	US-08-728-323A-1
7	52	2.6	3489	4	US-09-298-568-1
8	52	2.6	32207	2	US-08-770-379-20
9	52	2.6	32207	4	US-08-757-669A-20
10	52	2.6	32207	4	US-09-230-371A-20
11	44.2	2.2	51259	3	US-08-781-891-209
12	44	2.2	2887	2	US-08-533-306A-3
13	44	2.2	2887	2	US-08-742-923A-3
14	43.6	2.2	16442	3	US-08-182-175A-104
15	41.6	2.1	340	5	PCR-US92-06412-104
16	41.6	2.1	340	5	PCR-US92-06412-104
17	41	2.0	1926	4	US-09-249-585A-2
18	41	2.0	2580	3	US-09-050-863-2
19	41	2.0	2580	4	US-09-359-081-2
20	41	2.0	3432	2	US-09-130-114-1
21	41	2.0	9600	4	US-08-910-647-1
22	41	2.0	9600	4	US-09-620-925-1
23	41	2.0	10596	1	US-07-884-971-15
24	41	2.0	10596	1	US-07-885-971-15
25	41	2.0	10596	1	US-08-087-783A-15
26	41	2.0	10596	1	US-08-194-088B-15
27	41	2.0	10596	2	US-08-194-087-15

28	41	2.0	10596	5	PCR-US93-04648-15	Sequence 15, Appl
29	40	2.0	2223	1	US-08-317-522A-8	Sequence 8, Appl
30	40	2.0	2223	1	US-08-439-818A-8	Sequence 8, Appl
31	40	2.0	2223	2	US-08-751-965-8	Sequence 8, Appl
32	40	2.0	2223	2	US-08-738-975-8	Sequence 8, Appl
33	40	2.0	2223	2	US-08-728-626-8	Sequence 8, Appl
34	40	2.0	2223	3	US-08-808-599A-8	Sequence 8, Appl
35	39.2	2.0	15378	3	US-08-785-420-1	Sequence 16, Appl
36	39	1.9	456	2	US-08-557-309B-16	Sequence 16, Appl
37	39	1.9	456	3	US-08-834-306-16	Sequence 16, Appl
38	39	1.9	456	4	US-08-993-674A-16	Sequence 16, Appl
39	39	1.9	456	4	US-09-256-976-16	Sequence 16, Appl
40	38.8	1.9	1995	2	US-08-425-069-3	Sequence 3, Appl
41	38.8	1.9	1995	2	US-08-317-844B-3	Sequence 3, Appl
42	38.6	1.9	2793	1	US-08-209-747-1	Sequence 1, Appl
43	38.6	1.9	2793	1	US-08-458-298-1	Sequence 1, Appl
44	37.8	1.9	414	1	US-08-137-117D-85	Sequence 85, Appl
45	37.8	1.9	414	1	US-08-436-717-85	Sequence 85, Appl

ALIGNMENTS

RESULT 1
US-09-052-089A-7
; Sequence 7, Application US/09052089A
; Patent No. 6346605
; GENERAL INFORMATION:
; APPLICANT: Lee, Soo Y.
; TITLE OF INVENTION: SIGNAL TRANSDUCER FOR THE TNF RECEPTOR SUPER FAMILY, AND USES THEREOF
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,089A
; FILING DATE: 31-Mar-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-198 CIP 1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-052-089A-7
Query Match 100.0%; Score 2007; DB 4; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2007; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	1	GTGGGTGGAGCAAAATTGTAAGCAGAGCGAGCGCGCTCTACGAAGCCGGACCTGT	60
Db	1	GTGGGTGGAGCGAAATTTTAAGCAAGCGGAGCGGGGCGCTCTTAAGAGCCGGACCTGT	60
Oy	61	AGCAGTTTCTTTGGCTCTCTCTGGGCGCCCTTGTAGTCACAGCATCATGCTTTCGCTCTGT	120
Db	61	AGCAGTTTCTTTGGCTCTCTCTGGGCGCCCTTGTAGTCAGGCATCATGCTTTCGCTCTGT	120
Oy	121	TGCACATCTGTCTCCGACCTTCTTGATCACTCCCGGAGCTGGCGGCATCCACTGGGAC	180
Db	121	TGCACATCTGTCTCCGACCTTCTTGATCACTCCCGGAGCTGGCGGCATCCACACGGGAC	180
Oy	181	CACACCTTCGACCTTGCAGTGCCTTAATTCAGATCCCTTGTAGACAGACACCAAGTGGAGCTGC	240
Db	181	CACACCTTCGACCTTGCAGTGCCTTAATTCAGATCCCTTGTAGACAGACCAAGTGGAGCTGC	240
Oy	241	CCACAGTCCGGAATCCAGGTTTGGCAAAAGAACCATTAATCAATTAAGCTCTCTTTGATCTT	300
Db	241	CCACAGTCCGGAATCCAGGTTTGGCAAAAGAACCATTAATCAATTAAGCTCTCTTTGATCTT	300
Oy	301	GCCCAGAGGAGGAGGATGTCTTGATTCGGAATTCCTTAAAGATGAACCTGGACAAATGC	360
Db	301	GCCCAAGAGAGGAGGATGTCTTGATTCGGAATTCCTTAAAGATGAACCTGGACAAATGC	360
Oy	361	AGAGCCCAAGCTTTCCAGAAAAGACAAGGAGAAACGAGACGCGAGCTCATCTGCACT	420
Db	361	AGAGCCCAAGCTTTCCAGAAAAGACAAGGAGAAACGAGACGCGAGCTCATCTGCACT	420
Oy	421	CTGGGGGATACGCTGGAAAGAACGCAATGCTACTGTGTGTCTCTGACGACGCGCTTGGGC	480
Db	421	CTGGGGGATACGCTGGAAAGAACGCAATGCTACTGTGTGTCTCTGACGACGCGCTTGGGC	480
Oy	481	AAGCCGAGATGTCTGTCTCACACTGAAAAAACCAATGAATTAAGCTTAAAGACGACGAG	540
Db	481	AAGCCGAGATGTCTGTCTCACACTGAAAAAACCAATGAATTAAGCTTAAAGACGACGAG	540
Oy	541	GATGAGACCAAAACAGCACAAAGAGAGGCGGCGCGCTCAGAGCAAGATGAAGACCATG	600
Db	541	GATGAGACCAAAACAGCACAAAGAGAGGCGGCGCGCTCAGAGCAAGATGAAGACCATG	600
Oy	601	GAGCAGATTGAGCTTCTTACATCCAGAGCGACCTCCCTGAGSTGGAGAGATGATCCGAGAC	660
Db	601	GAGCAGATTGAGCTTCTTACATCCAGAGCGACCTCCCTGAGSTGGAGAGATGATCCGAGAC	660
Oy	661	ATGGGTGTGGACAGTCAGCGGTGGGAACAGCTGGCTGTGTACTGTGTCTCTCAAGAAA	720
Db	661	ATGGGTGTGGACAGTCAGCGGTGGGAACAGCTGGCTGTGTACTGTGTCTCTCAAGAAA	720
Oy	721	GAGTACGAGATCTTAAAGAGGCGACGGAAGGCGCTCAGGGGAGAGTGGCTACCAAGCTGAG	780
Db	721	GAGTACGAGATCTTAAAGAGGCGACGGAAGGCGCTCAGGGGAGAGTGGCTACCAAGCTGAG	780
Oy	781	AAGGATTTGTTTCTTCAGAAAGCAAGTTGGCAGACAGTCTACTCTGAATTTGGATCAGGCC	840
Db	781	AAGGATTTGTTTCTTCAGAAAGCAAGTTGGCAGACAGTCTACTCTGAATTTGGATCAGGCC	840
Oy	841	AAGTTAAACTGAAGTACGCCCGAAGAGCACTTACAGAGTGTCTGACAAAGAAATCTATGAGC	900
Db	841	AAGTTAAACTGAAGTACGCCCGAAGAGCACTTACAGAGTGTCTGACAAAGAAATCTATGAGC	900
Oy	901	CTGAAAAAAGAACTACAGATGTCTGCAAGAAACCTTAACTGCGACAGTGGCGACGTAG	960
Db	901	CTGAAAAAAGAACTACAGATGTCTGCAAGAAACCTTAACTGCGACAGTGGCGACGTAG	960
Oy	961	ACTGTGACCGCGCTGTGTTTAAAGAGCCAGCGCCCTGTGGAAGTGAATCTGAAGCTCGCG	1020
Db	961	ACTGTGACCGCGCTGTGTTTAAAGAGCCAGCGCCCTGTGGAAGTGAATCTGAAGCTCGCG	1020
Oy	1021	CGGCGCATCTTCCTGTGATGATATTTGATCTTCAATGCTACTCTTGTGATGTGGATCTCTCCCA	1080
Db	1021	CGGCGCATCTTCCTGTGATGATATTTGATCTTCAATGCTACTCTTGTGATGTGGATCTCTCCCA	1080

Qy	1081	GC	GGCGCCCTCCAGCTCCCGACGATGGTACTACGAAAAAATTGGCTAGAGAAAGCAAC	1140
Db	1081	GC	CGGGCCCTCCAGCTCCCGACGATGGTACTACGAAAAAATTGGCTAGAGAAAGCAAC	1140
Qy	1141	TC	CCCAATTCAGGATGTGCCAGAAATATGCAAGAGGCCCGAGAGAGATCCAGTC	1200
Db	1141	TC	CCCAATTCAGGATGTGCCAGAAAGATATGCAAGAGGCCCGAGAGAGATCCAGTC	1200
Qy	1141	TC	CCCAATTCAGGATGTGCCAGAAAGATATGCAAGAGGCCCGAGAGAGATCCAGTC	1200
Db	1141	TC	CCCAATTCAGGATGTGCCAGAAAGATATGCAAGAGGCCCGAGAGAGATCCAGTC	1200
Qy	1201	TC	ACGTGGGTGGCCAGAGCTGTGCAGAGAGACAGATGAGAACTGGTGGTCCCT	1260
Db	1201	TC	ACGTGGGTGGCCAGAGCTGTGCAGAGAGACAGATGAGAACTGGTGGTCCCT	1260
Qy	1261	AT	TTTTTGTCCGGAAATGCACTCTAGGCCAGAAAAACAGCCAAAAGGCCAGGTCAAGTC	1320
Db	1261	AT	TTTTTGTCCGGAAATGCACTCTAGGCCAGAAAAACAGCCAAAAGGCCAGGTCAAGTC	1320
Qy	1321	TC	TTTGCAGCAAAAGATGTGTAAAGACAGGCTTCGATGGGCTGGTGGCCGAGCAAAATTC	1380
Db	1321	TC	TTTGCAGCAAAAGATGTGTAAAGACAGGCTTCGATGGGCTGGTGGCCGAGCAAAATTC	1380
Qy	1381	AT	CCAGCTACTGCACACATCATGATCCGCCCATTTGGCTTTAAAGCCCAAGCAAGTT	1440
Db	1381	AT	CCAGCTACTGCACACATCATGATCCGCCCATTTGGCTTTAAAGCCCAAGCAAGTT	1440
Qy	1441	AAG	CAGAGGGTGAAGGTTGAAGACCGTCCCTCTCTTTCAGAGCCCAAGCTGACACCTTC	1500
Db	1441	AAG	CAGAGGGTGAAGGTTGAAGACCGTCCCTCTCTTTCAGAGCCCAAGCTGACACCTTC	1500
Qy	1501	CT	GTGTGTGTGAGAAACGTAGTCTACCAATATGGCCAGACATGCTGTCAACTGTATGG	1560
Db	1501	CT	GTGTGTGTGAGAAACGTAGTCTACCAATATGGCCAGACATGCTGTCAACTGTATGG	1560
Qy	1561	TCA	GAGACTGTCCAGGCGAGGTTTGTGGACAGAGCCCTACTTTCGGAGCACAGCCTGAAGT	1620
Db	1561	TCA	GAGACTGTCCAGGCGAGGTTTGTGGACAGAGCCCTACTTTCGGAGCACAGCCTGAAGT	1620
Qy	1621	GTA	GAGGCGACAAACAGGTGAGAGGTGTGTATGACACCCAGAGACTGCTTCTGCCCT	1680
Db	1621	GTA	GAGGCGACAAACAGGTGAGAGGTGTGTATGACACCCAGAGACTGCTTCTGCCCT	1680
Qy	1681	CAC	CTCCCACTCCCACTCGGAGGTGACATACCAAGCCCACTGATCTGTACAGA	1740
Db	1681	CAC	CTCCCTGCCCACTCCAGCACTGGGAGCTGACATBACCAAGCCCACTGATCTGTACAGA	1740
Qy	1741	GGT	CTCTCTGTGGCCAGGCTCTTGTATATAGCCATGATCAGATGTGTGACACTCTT	1800
Db	1741	GGT	CTCTCTCTGTGGCCAGGCTCTTGTATATAGCCATGATCAGATGTGTGACACTCTT	1800
Qy	1801	CT	GAGGCTCGAGACACAGCTACTTGTATGATCTCTGTGGACCAAGTCTGTAGGCA	1860
Db	1801	CT	GAGGCTCGAGACACAGGTCACCTTGTATGATCTCTGTGGACCAAGTCTGTAGGCA	1860
Qy	1861	TC	TAGCAGCAGCTACAGCCCAAGCTTCTACCTGCTTGAATAGCATAGGCTGG	1920
Db	1861	TC	TAGCAGCAGCTACAGCCCAAGCTTCTACCTGCTTGAATAGCATAGGCTGG	1920
Qy	1921	GCC	AAGCAGGGTGGGAAATGAGATAGACATGGATGTATGAGAGAGATGAAGATTTT	1980
Db	1921	GCC	AAGCAGGGTGGGAAATGAGATAGACATGGATGTATGAGAGAGATGAAGATTTT	1980
Qy	1981	CCC	GAIAAAAAAAAAAAAAAAAAAAAAA	2007
Db	1981	CCC	GAIAAAAAAAAAAAAAAAAAAAAAA	2007

RESULT 2
US-08-968-751-1
: Sequence 1, Application us/08968751
: Patent NO. 5946643
: GENERAL INFORMATION:
: APPLICANT: Rudinfield, Bonnie
: APPLICANT: Polakiss, Paul G.
: APPLICANT: Lichtenfelser, Carol

APPLICANT: Vuong, Terilyn T.
TITLE OF INVENTION: MODULATORS OF BRCA1 ACTIVITY
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 3031 Research Drive
CITY: Richmond
STATE: CA
COUNTRY: USA
ZIP: 94806
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,751
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Giotta, Gregory
REGISTRATION NUMBER: 32,028
REFERENCE/DOCKET NUMBER: ONYX1024 GG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 262-8710
TELEFAX: (510) 222-9758
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2065 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 103..1512
US-08-968-751-1

Query Match 94.2%; Score 1890.8; DB 2; Length 2065;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1946; Conservative 0; Mismatches 17; Indels 5; Gaps 4;

44 TAGAAGCCGAGCTGAGCAGTTCTTGGCTGGCCGCGCCCTTGAGTCCAGCCATCA 103
|||||
44 TAGAAGCCGAGCTGAGCAGTTCTTGGCTGGCCGCGCCCTTGAGTCCAGCCATCA 103
DB 44 TAGAAGCCGAGCTGAGCAGTTCTTGGCTGGCCGCGCCCTTGAGTCCAGCCATCA 103
104 TGCTATCCGCTGCTGTGTCATATCTGTCGACATCTTCTTGATGATCTCCCGGACGTGG 163
|||||
104 TGCTATCCGCTGCTGTGTCATATCTGTCGACATCTTCTTGATGATCTCCCGGACGTGG 163
DB 104 TGCTATCCGCTGCTGTGTCATATCTGTCGACATCTTCTTGATGATCTCCCGGACGTGG 163
164 CCGCCATCCACTCGGCGCACACCTTCCACTTGCAGTGCCCTAATTCAGTTGAGACAG 223
|||||
164 CCGCCATCCACTCGGCGCACACCTTCCACTTGCAGTGCCCTAATTCAGTTGAGACAG 223
DB 164 CCGCCATCCACTCGGCGCACACCTTCCACTTGCAGTGCCCTAATTCAGTTGAGACAG 223
224 CACCAAGTGGAGCTGGCCAGTGGCCAGTCCAGTTCAGTTGCAAAAGAACATATCATATA 283
|||||
224 CACCAAGTGGAGCTGGCCAGTGGCCAGTTCAGTTCAGTTGCAAAAGAACATATCATATA 283
DB 224 CACCAAGTGGAGCTGGCCAGTGGCCAGTTCAGTTCAGTTGCAAAAGAACATATCATATA 283
284 AGCTCTCTTTGATCTTGGCCAGAGAGAGATGCTTGATGATCGAATTCCTTAAGA 343
|||||
284 AGCTCTCTTTGATCTTGGCCAGAGAGAGATGCTTGATGATCGAATTCCTTAAGA 343
DB 284 AGCTCTCTTTGATCTTGGCCAGAGAGAGATGCTTGATGATCGAATTCCTTAAGA 343
344 ATGAACCTGGACATGTGACAGCCAGCTTTCCAGAAAGCAAGAGAAACGACAGCC 403
|||||
344 ATGAACCTGGACATGTGACAGCCAGCTTTCCAGAAAGCAAGAGAAACGACAGCC 403
DB 344 ATGAACCTGGACATGTGACAGCCAGCTTTCCAGAAAGCAAGAGAAACGACAGCC 403
404 AGGTGATCATGACACACTGCGGGGATACGCTGGAAGAAGCAATGCTACGTGGTATCTC 463
|||||
404 AGGTGATCATGACACACTGCGGGGATACGCTGGAAGAAGCAATGCTACGTGGTATCTC 463
DB 404 AGGTGATCATGACACACTGCGGGGATACGCTGGAAGAAGCAATGCTACGTGGTATCTC 463
464 TGCAGCAGGCTTGGGCAAGCGCAGATGCTGTCTCCACATGAAAAAGCAGATGAGT 523
|||||

|||||
DB 464 TGCAGCAGGCTTGGGCAAGCGCAGATGCTGTCTCCACATGAAAAAGCAGATGAGT 523
464 TGCAGCAGGCTTGGGCAAGCGCAGATGCTGTCTCCACATGAAAAAGCAGATGAGT 523
DB 464 TGCAGCAGGCTTGGGCAAGCGCAGATGCTGTCTCCACATGAAAAAGCAGATGAGT 523
524 ACTTAGAGCAGCAGCAGATGAGACCAACAAACAGCAGAGAGGCGGCGCTCAGGA 583
|||||
524 ACTTAGAGCAGCAGCAGATGAGACCAACAAACAGCAGAGAGGCGGCGCTCAGGA 583
DB 524 ACTTAGAGCAGCAGCAGATGAGACCAACAAACAGCAGAGAGGCGGCGCTCAGGA 583
584 GCAAGATGAAGACCATGAGACAGATTGAGCTTCTACTCCAGAGCCAGCTCAGAGGTGG 643
|||||
584 GCAAGATGAAGACCATGAGACAGATTGAGCTTCTACTCCAGAGCCAGCTCAGAGGTGG 643
DB 584 GCAAGATGAAGACCATGAGACAGATTGAGCTTCTACTCCAGAGCCAGCTCAGAGGTGG 643
644 AGGAGATGATCCGAGACATGGGTGTGGACAGTCCAGCGGCTGGAACAGCTGTGTACT 703
|||||
644 AGGAGATGATCCGAGACATGGGTGTGGACAGTCCAGCGGCTGGAACAGCTGTGTACT 703
DB 644 AGGAGATGATCCGAGACATGGGTGTGGACAGTCCAGCGGCTGGAACAGCTGTGTACT 703
704 GTGTGTCTCAGAAAGAAAGTACGAGATCTAAAGAGCAGCAGAAAGCCTCAGGGAGG 763
|||||
704 GTGTGTCTCAGAAAGAAAGTACGAGATCTAAAGAGCAGCAGAAAGCCTCAGGGAGG 763
DB 704 GTGTGTCTCAGAAAGAAAGTACGAGATCTAAAGAGCAGCAGAAAGCCTCAGGGAGG 763
764 TGCTGACAGCTGAGGAAGATTTGTTTCCCTCCAGAACCAAGTTCAGACAGTACT 823
|||||
764 TGCTGACAGCTGAGGAAGATTTGTTTCCCTCCAGAACCAAGTTCAGACAGTACT 823
DB 764 TGCTGACAGCTGAGGAAGATTTGTTTCCCTCCAGAACCAAGTTCAGACAGTACT 823
824 CTGAATTGATCAGGCCCAAGTTAGAACTGAACTGAGCCAGAAAGACTTACAGAGTCTG 883
|||||
824 CTGAATTGATCAGGCCCAAGTTAGAACTGAACTGAGCCAGAAAGACTTACAGAGTCTG 883
DB 824 CTGAATTGATCAGGCCCAAGTTAGAACTGAACTGAGCCAGAAAGACTTACAGAGTCTG 883
884 ACAAGGAATCATGACCTTAAAAAAGAGTAAAGATCTGTCAGAGAAACCTTGACCTGC 943
|||||
884 ACAAGGAATCATGACCTTAAAAAAGAGTAAAGATCTGTCAGAGAAACCTTGACCTGC 943
DB 884 ACAAGGAATCATGACCTTAAAAAAGAGTAAAGATCTGTCAGAGAAACCTTGACCTGC 943
944 CACAGAGGCGCAGTGAAGCTGTGACCGCTGGTTTAAAGAGCCAGCCCTGTGGAGG 1003
|||||
944 CACAGAGGCGCAGTGAAGCTGTGACCGCTGGTTTAAAGAGCCAGCCCTGTGGAGG 1003
DB 944 CACAGAGGCGCAGTGAAGCTGTGACCGCTGGTTTAAAGAGCCAGCCCTGTGGAGG 1003
1004 TGAATCTGAAGCTCCGCGGCGCATCTTCCGTGATGATGATCTCAATGCTACCTTTG 1063
|||||
1004 TGAATCTGAAGCTCCGCGGCGCATCTTCCGTGATGATGATGATCTCAATGCTACCTTTG 1063
DB 1004 TGAATCTGAAGCTCCGCGGCGCATCTTCCGTGATGATGATGATCTCAATGCTACCTTTG 1063
1064 ATGTGATACTCCCGCCAGCCGCGCTCCAGCTCCAGCATGTGTACTGAAAAACTTT 1123
|||||
1064 ATGTGATACTCCCGCCAGCCGCGCTCCAGCTCCAGCATGTGTACTGAAAAACTTT 1123
DB 1064 ATGTGATACTCCCGCCAGCCGCGCTCCAGCTCCAGCATGTGTACTGAAAAACTTT 1123
1124 GCTAGAGAGTCAACATCCCAATTCAGATGTCCCAAGAGATGTGAAGGCCCA 1183
|||||
1124 GCTAGAGAGTCAACATCCCAATTCAGATGTCCCAAGAGATGTGAAGGCCCA 1183
DB 1124 GCTAGAGAGTCAACATCCCAATTCAGATGTCCCAAGAGATGTGAAGGCCCA 1183
1184 GGAAGAGTCCAGCTCTCACTGAGTGGCCAGAGCTGTGAGAGAGACAGATGAGGAAC 1243
|||||
1184 GGAAGAGTCCAGCTCTCACTGAGTGGCCAGAGCTGTGAGAGAGACAGATGAGGAAC 1243
DB 1184 GGAAGAGTCCAGCTCTCACTGAGTGGCCAGAGCTGTGAGAGAGACAGATGAGGAAC 1243
1244 TGCTGCTGCTTCCCTATTTTGTCCGGAATGCCATCTTGAAGCCAGAAACCCCAAA 1303
|||||
1244 TGCTGCTGCTTCCCTATTTTGTCCGGAATGCCATCTTGAAGCCAGAAACCCCAAA 1303
DB 1244 TGCTGCTGCTTCCCTATTTTGTCCGGAATGCCATCTTGAAGCCAGAAACCCCAAA 1303
1304 GGCACAGGTGAGAGTCTCTTGCAGCAAGATGTGAAGAGAGAGTTCGATGAGGTGG 1363
|||||
1304 GGCACAGGTGAGAGTCTCTTGCAGCAAGATGTGAAGAGAGAGTTCGATGAGGTGG 1363
DB 1304 GGCACAGGTGAGAGTCTCTTGCAGCAAGATGTGAAGAGAGAGTTCGATGAGGTGG 1363
1364 GTGGCCGCAAAATTCATCAGCTTACTGACACAGTCAATCCGCCATTCCTCTTGA 1423
|||||
1364 GTGGCCGCAAAATTCATCAGCTTACTGACACAGTCAATCCGCCATTCCTCTTGA 1423
DB 1364 GTGGCCGCAAAATTCATCAGCTTACTGACACAGTCAATCCGCCATTCCTCTTGA 1423
1424 AGCCCAAGCAAGGTTAAGCAGAGGTGAGGTTGAAGAGCCGTCTCTCTTCCAGG 1483
|||||
1424 AGCCCAAGCAAGGTTAAGCAGAGGTGAGGTTGAAGAGCCGTCTCTCTTCCAGG 1483
DB 1424 AGCCCAAGCAAGGTTAAGCAGAGGTGAGGTTGAAGAGCCGTCTCTCTTCCAGG 1483
1484 CCAAGCTGACACCTTCTGTGTGCTGAGAACAGTGAAGTGCACATGACCAGACACA 1543
|||||
1484 CCAAGCTGACACCTTCTGTGTGCTGAGAACAGTGAAGTGCACATGACCAGACACA 1543
DB 1484 CCAAGCTGACACCTTCTGTGTGCTGAGAACAGTGAAGTGCACATGACCAGACACA 1543
1544 TGCTGCAACTGTAGTCTCAAGAGACTGTCAGGAGG--TTTGTGAGCAGAGCCCTACT 1601
|||||

Db 1544 TGCCTCAACTTGTAGTCAAGAGCTGTCCAGGAGGGGTTTGTGACAGACCCCACT 1603
 QY 1602 TTGGGACACAGCTGAGTGTAAAGGACAGCAAAAGAGTGGGTGAGTGAACCCAG 1661
 Db 1604 TTGGGACACAGCTGAGTGTAAAGGACAGCAAAAGAGTGGGTGAGTGAACCCAG 1663
 QY 1662 AGACTGCTCTTCCCTGCGCTCAGCCCTGCGCCACTCTACAGACTGGAGCTCAATGACCA 1721
 Db 1664 AGACTGCTCTTCCCTGCGCTCAGCCCTGCGCCACTCTACAGACTGGAGCTCAATGACCA 1723
 QY 1722 CCCACGATCTGTCAAGAGCTCTGT-CTGTGCGAGCTCTGTGTTATACCATGAT 1780
 Db 1724 CCCACGATCTGTCAAGAGCTCTGT-CTGTGCGAGCTCTGTGTTATACCATGAT 1783
 QY 1781 CAGATGTGTCAAGAGCTCTGTGCGCTGAGACAGAGTCACTGTGTTAGTCTGTCTGT 1840
 Db 1784 CAGATGTGTCAAGAGCTCTGTGCGCTGAGACAGAGTCACTGTGTTAGTCTGTCTGT 1843
 QY 1841 GACACAGAGTGTGAGGCTCTCAAGCAGCCTCAGCCCAAGCTTCTACCTGCTTTGAC 1900
 Db 1844 GACACAGAGTGTGAGGCTCTCAAGCAGCCTCAGCCCAAGCTTCTACCTGCTTTGAC 1903
 QY 1901 TTGCTCTTA-GCATAGCTTGGCCAGCAGAGTGGGGAATGAGATAGCATGGATCT 1959
 Db 1904 TTGCTCTTAAGGCTAGCTGGGCGCAAGCAGGTTGGGGAATGAGATAGCATGGATCT 1962
 QY 1960 ATGAGAGAGTGAAGATTTTCCGAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 2007
 Db 1963 ATGAGAGAGTGAAGATTTTCAATGTAATAATTTTAAAAAATTTTAAAAAATTTTAAAAA 2010

RESULT 3
 US-09-052-089A-8
 : Sequence 8, Application US/09052089A
 : Patent No. 6346605

GENERAL INFORMATION:

APPLICANT: Lee, Soo Y.

Choi, Yongwon

TITLE OF INVENTION: SIGNAL TRANSDUCER FOR THE TNF RECEPTOR SUPER

FAMILY, AND USES THEREOF

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/052,089A

FILING DATE: 31-Mar-1998

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-198 CIP 1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1975 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

; ORIGINAL SOURCE:
 ; ORGANISM: mouse
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-09-052-089A-8

Query Match 53.0%; Score 1062.8; DB 4; Length 1975;
 Best Local Similarity 74.6%; Pred. No. 3.3e-289;
 Matches 1506; Conservative 0; Mismatches 447; Indels 65; Gaps 11;

QY 1 GTGGGTTGAGGCAAAATTTGAACAGCGAGCGGGGCG--GCTTACGAGACCGGCACT 58
 Db 9 GTGGGTTGAGGCAAAATTTGAACAGCGAGCGGGGCGGTTCACCAAACTGTGTCT 68
 QY 59 GTAGCAATTTCTTGGCTCCCTGGCCCTTGTAGTGCAGCATCATGCTTATCCGTCTC 118
 Db 69 GTCTCTG-AGAGCTGTTCCTCGCTGCTGTGAGTGCAGCATCATGCTTATCCGTCTC 127
 QY 119 TGTGCACTATCTGCTCCGACTTCTTGATCACTCCCGCAGCTGGCCGCAATCCAGTGG 178
 Db 128 TGTGCACTATCTGCTCCGACTTCTTGATCACTCCCGCAGCTGGCCGCAATCCAGTGG 187
 QY 179 GCCACACCTTCCACTGGAGTGGCTTAATTCAGTCTTGTAGACAGCAGCAAGTGGAGCT 238
 Db 188 GCCACACCTTCTTCTGCAATGCTTATCCAGTGTGAGACAGCAGCAAGTGGAGCT 247
 QY 239 GCCACAGTGGCCGATTCAGGTTGGCAAAAAGAACATTTATCATTAAGCTTTTGTATC 298
 Db 248 GCCACAGTGTGATATTCAGGTTGGCAAAAAGAACATTTATTAACAACTTTCTTTGACC 307
 QY 299 TTGCCAGAGAGAGGAATGCTTGTGATCGAATTTTAAAGATGAATGAGACGACATG 358
 Db 308 TTGCCAGAGAGAGGAATGCTTGTGATCGAATTTTAAAGATGAATGAGACGACG 367
 QY 359 TCAGAGCCCAAGCTTTCGCAAAAAGACAGAGAAAGACAGACGCCAGTCAATCAGACA 418
 Db 368 TCAGAGCCCAAGCTTTCGCAAAAAGACAGAGAAAGACAGACGCCAGTCAATCAGACA 427
 QY 419 CTTGCGGATACGCTGGAAGAAAGCAATGCTTATCTGATCTGCAAGAGCTTTGG 478
 Db 428 CTTGCGGATACGCTGGAAGAAAGCAATGCTTATCTGATCTGCAAGAGCTTTGAA 487
 QY 479 GCAAGCCCAAGATGCTGCTCCACACTGAGAAAAAGAGATGAATGAGACGACGAC 538
 Db 488 GCAAGCCCAAGATGCTGCTCCACACTGAGAAAAAGAGATGAATGAGACGACGAC 547
 QY 539 AGGATGAGACCAAGACAGACAAAGAGAGGCGGGGCTCAGGACCAAGATGAAGACA 598
 Db 548 AGGATGAGACCAAGACAGCTCGGAGAGAGGCCACCGACTCAAGTCAAGATGAAGACA 607
 QY 599 TGGAGCAGATTGAGCTTCTACTTCAGAGCCAGCTCCCTGAGTGGAGAGATGATCCGAG 658
 Db 608 TGGAGCAGATTGAGCTTCTACTTCAGAGCCAGCTCCCTGAGTGGAGAGATGATCCGAG 667
 QY 659 ACATGGGTGGGACAGTACAGCGGTGGAACAGCTGCTGTACTGTCTCTCAGACA 718
 Db 668 ACATGGGTGGGACAGTACAGCGGTGGAACAGCTGCTGTACTGTCTCTCAGACA 727
 QY 719 AAGAGTACGAGATCTAAAGAGGACAGAGGCGCTCAGGGGAGGTGGTGAACAGCTGA 778
 Db 728 AAGAGTACGAGATCTAAAGAGGACAGAGGCGCTCAGGGGAGGTGGTGAACAGCTGA 787
 QY 779 GGAAGATTTGTTTCTCCAGAGCAAGTTGAGACAGTCTACTCTGATGATGATCAGAG 838
 Db 788 GGAAGATTTGTTTCTCCAGAGCAAGTTGAGACAGTCTACTCTGATGATGATCAGAG 847
 QY 839 CCAAGTTAGACTGAAGTACGCCAGAGCAAGTCTACAGAGTCTGCAAGAAATCATGA 898
 Db 848 CCAAGTTAGACTGAAGTACGCCAGAGCAAGTCTACAGAGTCTGCAAGAAATCATGA 907
 QY 899 GCCTGAAAAAAGAG-CTAAGATGCTGCGAGAAACCTTAACCTGACCAAGTGGCACT 957
 Db 908 GCCTGAAAAAAGAGTCTGATGATCTCCAGAGGAACCTTGAGCTGCTCC-CCGACCAAT 966

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PT99pt-F15
US-08-232-463-14

Query Match	3.3%;	Score 65.8;	DB 1;	Length 7218;
Best Local Similarity	4.7%;	Pred. No. 2.1e-08;		
Matches	19;	Conservative 230;	Mismatches 152;	Indels 0;
			Gaps	0;

[illegible]

RESULT 6
US-08-728-323A-1

Sequence: Application US/06/26325A
Patent No. 5948676
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DAT: :
APPLICATION NUMBER: US/08/728,323A
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28, 678
REFERENCE/DOCKET NUMBER: 0575/52268/JPM/MSC/SKSS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: CDS
LOCATION: 1..3489
US-08-728-323A-1

Query Match	2.68;	Score 52;	DB 2;	Length 3489;
Best Local Similarity	48.98;	Pred. No.	0.00011;	
Matches 139;	Conservative	0;	Mismatches 145;	Indels 0;
			Gaps	0;

[illegible]

RESULT 7

Sequence 1, Application US/09298568
Patent No. 6322792
GENERAL INFORMATION:
APPLICANT: Kieff, Elliott D.
APPLICANT: Ballesta, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19

Accession	Sequence	Position
Db	572 GCCAGGCCCAACGACGAGGTGGACATTAAGAAAGAAAGAGCTGGAGCGCCACGTGGCAGGAGC	6313
Qy	650 TGCATCCGAGACATGAGTGTGGGAACAGTCAGCGGTGGAAACAGTGGCTGTGTACTGTGTGT	7089
Db	632 TGCAGTCCCAAGTCGACGCCATGGGAGGGGGCCCGGGGGAGCACTTAATGACAAATCCACA	6911
Qy	710 CTCCTCAAGAAAGAGTACGAGAAATCTAAAGAAGGACGCGAAGGCTTCAGGGGAGGTGGCTG	7639
Db	692 AGCTGCAGAAATGAAGTTGAGAGCGCTACAGAGGATGCTTAAAGAGCGCGAGGGAGAAAGCCA	7511
Qy	770 ACAAGCTGAGGAGAGATTGTTTTCCTTCACAGAACCAAGTTGCCAG	813
Db	752 TTAAAGCTGGCCACGAGACGTGGCGTCCCTCACTATCTCCACAGTCCAG	795

RESULT 14

US-08-781-208/C
Sequence 208, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-Eu
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4300
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-208

Query Match	2.2%	Score 43.6	DB 3	Length 16442
Best Local Similarity	47.4%	Pred. No. 0.057		
Matches 130; Conservative	0	Mismatches 144	Indels 0	Gaps 0

[illegible][illegible]

RESULT 15

```

US-08-182-175A-104
; Sequence 104, Application US/08182175A
; Patent No. 5559223
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containin
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182.175A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELE: 835420
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: E. coli
; CELL TYPE: DH5 alpha
; IMMEDIATE SOURCE:
; CLONE: segment 534 [seg 534]
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..326
; OTHER INFORMATION: /function= "synthetic seed storage protein"
; OTHER INFORMATION: /product= "protein"
; OTHER INFORMATION: /gene= "ssp"
; OTHER INFORMATION: /standard_name= "SSP-534"
US-08-182-175A-104

```

Query Match	2.18	Score 41.6	DB 1	Length 340
Best Local Similarity	46.88	Pred. No. 0.031		
Matches 131; Conservative	0	Mismatches 149	Indels 0	Gaps 0

THIS PAGE BLANK (USPTO)